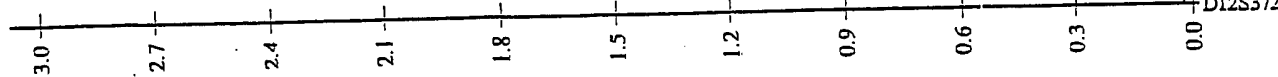


162 cM



- D12S357  
 - D12S392  
 - D12S97 D12S1045  
 - D12S1659  
 - D12S2078  
 - D12S324  
 - D12S342  
 - D12S300  
 - FLA2G1B D12S395  
 - D12S385  
 - D12S366 D12S1619  
 - D12S2070  
 - D12S1341 NOS1  
 - D12S811  
 - D12S78  
 - D12S360 D12S338  
 - IGF1 PAH  
 - D12S1727 D12S1607  
 - D12S1706 D12S1300  
 - D12S95 D12S829  
 - D12S1064  
 - D12S82 D12S819  
 - D12S379 D12S311  
 - D12S64  
 - D12S326  
 - D12S1052 D12S92  
 - D12S43  
 - IFNgamma D12S375  
 - D12S1294  
 - D12S83  
 - D12S398  
 - D12S368  
 - GATA91H06  
 - D12S1042  
 - D12S373  
 - D12S364  
 - D12S91 D12S358  
 - D12S77  
 - GATA49D12

Figure 1

**Gene 214**

B0702C13A1x  
A005Q05  
Th  
B0702C13A1y

RP11-0702C13

Figure 2

10 30 50  
 TCACGAGCTGCCACGTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCACGTCG  
 T S C P R P L Q E G T P G S R A A H V V

70 90 110  
 TCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCACGTCCTCTCCAGGAAGGACCCGGG  
 S R K G P G S T S C P R P L Q E R T R V

130 150 170  
 TCCACGAGCTGGCCACGTCCTCTGCAGGAAGGGACCCCGGGTCCACGAGCTGCCACGTC  
 H E L A T S S A G R D P G S T S C P R P

190 210 230  
 CTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCACGTCCTCTCCAGGAAGGGACCC  
 L Q E G T P G S R A A H V L S R K G P R

250 270 290  
 GGGTCCACGAGCTGCCACGTCCTCTCCAGGAAGGGACCCCGGGTCCACGAACTGCCAC  
 V H E L P T S S P G R D P G S T N C P R

310 330 350  
 GTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCACGTCCTCTCCAGGAGGGGAC  
 P L Q E G T P G S R A A H V L S R R G H

370 390 410  
 ACCGGGTTCACGAGCTGCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCATGAGCTGCC  
 R V H E L P T P S P G R D P G F M S C P

430 450 470  
 CACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCACGCCCTCTCCAGGAGGGG  
 R P L Q E G T R V H E L P T P S P G G D

490 510 530  
 ACCCGGGTCCACGAGCTGCCACGTCGTCACGGAAGGGACCCCGGGTCCACGAGCTGCC  
 P G P R A A H V V N G K G P G S T S C P

Figure 3A



1090 1110 1130  
TGGCGCCTCGGTGCGCAGCCTTGGACCTGCCCCATGGACCTGGGAACCTCCCGGCTCTT  
A P R C A A L D L P P W T W E P P G S S

1150 1170 1190  
CCCACTCGGGAAAGGAAGGCTCTGGGCATGGAGGTCGGCCAGGCCCCATCCCCGTACCCT  
H S G K E G S G H G G R P G P I P V P W

1210 1230 1250  
GGCCCTTCTTCTGCTTCCTGTTTGTCACTGCCCCGGGGCCTTTGCACCTGCATTCCCTC  
P F F L L P V C H C P G A F A P A F P L

1270 1290 1310  
TCTCTAGACAGGGTTTCTCCTCATTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGACGA  
S R Q G F S S L A R L V S N S \*

1330 1350 1370  
TCCACCTGCCTCAGCCTCCCGAAGTGTTGGGATTACAGGCACGAGCCACTGTGCCCGGCC

1390 1410 1430  
ATCATTCCTTTTTACTGCTGACTAATAGTCTGCTGTGTGAATCCACCGCTAGAAA.CCCAC

1450 1470 1490  
TCATCAGTTGATGGTCATGTGGGTTGCTTCTGCTATTCGCTTATTATGAACAGTGCTGGA

1510 1530 1550  
ATAAACGTTCTGTGCACTCTTGGGCATACGCCTAGGAGTGGAAGTCTGGGTCAAAAAA

1570  
AAAAAAAAAAAAAAAAAAAAA

Figure 3C

10 30 50  
 TCACGAGCTGCCACGTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCACGTCG  
 T S C P R P L Q E G T P G S R A A H V V

70 90 110  
 TCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCACGTCCTCTCCAGGAAGGACCCGGG  
 S R K G P G S T S C P R P L Q E R T R V

130 150 170  
 TCCACGAGCTGGCCACGTCCTCTGCAGGAAGGGACCCCGGGTCCACGAGCTGCCACGTC  
 H E L A T S S A G R D P G S T S C P R P

190 210 230  
 CTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCACGTCCTCTCCAGGAAGGGACCC  
 L Q E G T P G S R A A H V L S R K G P R

250 270 290  
 GGGTCCACGAGCTGCCACGTCCTCTCCAGGAAGGGACCCCGGGTCCACGAACTGCCAC  
 V H E L P T S S P G R D P G S T N C P R

310 330 350  
 GTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCACGTCCTCTCCAGGAGGGGAC  
 P L Q E G T P G S R A A H V L S R R G H

370 390 410  
 ACCGGGTTCACGAGCTGCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCATGAGCTGCC  
 R V H E L P T P S P G R D P G F M S C P

430 450 470  
 CACGTCCTCTCCAGGAAGGGACCCCGGGTCCACGAACTGCCACGCCCTCTCCAGGAGGGG  
 R P L Q E G T R V H E L P T P S P G G D

490 510 530  
 ACCCGGGTCCACGAGCTGCCACGTCGTCACGGGAAGGGACCCCGGGTCCACGAGCTGCC  
 P G P R A A H V V N G K G P G S T S C P

550 570 590

Figure 4A

CACGTCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCCACGCGCTCTCCAGGAGGGG  
R P L Q E G T R V H E L P T R S P G G D

610 630 650  
ACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTG  
T G F T S C P R P L Q E G T P G S R A A

670 690 710  
CCCACGTCTCTCCAGGAGGGGACACCGGGTTCACGAGCTGCCCACGTCTCTCCAGGAG  
H V L S R R G H R V H E L P T S S P G G

730 750 770  
GGGACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAGGGGACACCGGGTTCACGAG  
D T G F T S C P R P L Q E G T P G S R A

790 810 830  
CTGCCCACGTCTCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCTCTCCAGG  
A H V L S R K G P G S T S C P R P L Q E

850 870 890  
AGGGGACACCGGGTTCACGAGCTGCCCACGCACTTTCCAGGAAGGGACCCCGGGTTCAGG  
G T P G S R A A H A L S R K G P R V Q V

910 930 950  
TCTCCTGCCGGCCACATCGTGCCTTTGTGTAAATCAGAAGAAAGATGAGGAACAGGCC  
S C R P T S C L C V N Q K K D E E Q A L

970 990 1010  
TCCTCTCTCTCCAGGCAGGCTTTGGTGGAGGGGCTGGATCTCCTGCCGCACCTTCCCTGG  
L S L Q A G F G G G A G S P A A P S L A

1030 1050 1070  
CAGGGCACCCCTGTGCTTGAGCCCCAGAACTGCAGGCGGCCGGCAGAGAAGGGGTTCATGA  
G H P V L E P Q N C R R P A E K G S M M

1090 1110 1130  
TGGCGCCTCGGTGCGCAGCCTTGACCTGCCCCATGGACCTGGAGACAGGGTTTCTCCT  
A P R C A A L D L P P W T W R Q G F S S

Figure 4B

[illegible]

Figure 4C



10 30 50  
 TCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCG  
 T S C P R P L Q E G T P G S R A A H V V

70 90 110  
 TCTCCAGGAAGGGACCCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAAGGACCCGGG  
 S R K G P G S T S C P R P L Q E R T R V

130 150 170  
 TCCACGAGCTGGCCACGTCCTCTGCAGGAAGGGACCCCGGGTCCACGAGCTGCCCACGTC  
 H E L A T S S A G R D P G S T S C P R P

190 210 230  
 CTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCC  
 L Q E G T P G S R A A H V L S R K G P R

250 270 290  
 GGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTCCACGAACTGCCCAC  
 V H E L P T S S P G R D P G S T N C P R

310 330 350  
 GTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAGGGGAC  
 P L Q E G T P G S R A A H V L S R R G H

370 390 410  
 ACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCATGAGCTGCC  
 R V H E L P T P S P G R D P G F M S C P

430 450 470  
 CACGTCCTCTCCAGGAAGGGACCCCGGGTCCACGAACTGCCCACGCCCTCTCCAGGAGGGG  
 R P L Q E G T R V H E L P T P S P G G D

490 510 530  
 ACCCGGGTCCACGAGCTGCCCACGTCGTCACGGGAAGGGACCCCGGGTCCACGAGCTGCC  
 P G P R A A H V V N G K G P G S T S C P

Figure 5A

[illegible]

Figure 5B

[illegible]

Figure 5C

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

Figure 6A

[illegible]

Figure 6B

1090                      1110                      1130  
 TGGCGCCTCGGTGCGCAGCCTTGGACCTGCCCCATGGACCTGGATGCCAGTGATGCCTG  
 A P R C A A L D L P P W T W M P V M P E

1150                      1170                      1190  
 AGGTCTGCAGGGCAGTGCATACGCTCACCGCCTGGCCGCTCAGGAGCCTGTGCTTGACCC  
 V C R A V H T L T A W P L R S L C L T P

1210                      1230                      1250  
 CCAAATCCGCCCCCAACTCCCTGTTACCGGCTCACTCCTTCCATGAGGGGCCTTCCCCA  
 K S A P Q L P V T G S L L P \*

1270                      1290                      1310  
 GGGACAGCCGATGCTCTCCTGATGGCTCCTGCCCTTGACAGTGCTGCCCCGCTTGCCC

1330                      1350                      1370  
 ACCTGGCCTGGACCCCTCGCCTGAGCCCCCTCAGGGCTCTGCGCCACCTCAACCCAGGCGT

1390                      1410                      1430  
 TTGTTCCGCAGGAACCTCCCGGCTCTTCCCACTCGGGAAAGGAAGGCTCTGGGCATGGAG

1450                      1470                      1490  
 GTCGGCCAGGCCCCATCCCCGTACCCTGGCCCTTCTTCTGCTTCTGTTTGTCACTGCC

1510                      1530                      1550  
 CCGGGGCCTTTGCACCTGCATTCCCTCTCTGTGAGTGTCTGCGGGCCCGTTACCCACG

1570                      1590                      1610  
 TCACCGTCCCAGGATACCTTTTCTTTCTTCTCTCTCTCCAGCTTTATTGAGGTATAGT

1630                      1650                      1670  
 TGACAATTGAGGACGGTGTGCACTCAAGGTATGCAGCATCACAACTGACACACGTAGGC

1690                      1710                      1730  
 ATGTGAAATGAGTCCCACAATTGGGCTAATTAACACACCCATCACCTTACATGGTTACT

Figure 6C

1750                      1770                      1790  
 TCTTTCTGTGGTGAGAACAATAAATTTAAATAGAGGACACACAGCCTGGGCAACATAGT  
 1810                      1830                      1850  
 GAGACCCTGTCTCTACAAATATAAAAAATTATCTGGACGTGGTGGTGCACACCTGTGGT  
 1870                      1890                      1910  
 CCCAGCTACTTGGGAAGCTGAGGCTGGAGAATCACTTGAGCCTGGGAGGCGGAGGTTGCG  
 1930                      1950                      1970  
 GTGCACTCCAGCCTGGGCGACAGAGGGAGGCCCTATCTCAAATAAAATAAAAGGACA  
 1990                      2010  
 CATTCTTATCAAAAAAAAAAAAAAAAAAAAAA

Figure 6D

10 30 50  
 TCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCG  
 T S C P R P L Q E G T P G S R A A H V V

70 90 110  
 TCTCCAGGAAGGGACCCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCGGG  
 S R K G P G S T S C P R P L Q E R T R V

130 150 170  
 TCCACGAGCTGGCCACGTCCTCTGCAGGAAGGGACCCCGGGTCCACGAGCTGCCCACGTC  
 H E L A T S S A G R D P G S T S C P R P

190 210 230  
 CTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCG  
 L Q E G T P G S R A A H V L S R K G P R

250 270 290  
 GGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTCCACGAACTGCCCAC  
 V H E L P T S S P G R D P G S T N C P R

310 330 350  
 GTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAGGGGAC  
 P L Q E G T P G S R A A H V L S R R G H

370 390 410  
 ACCGGGTTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCATGAGCTGCC  
 R V H E L P T P S P G R D P G F M S C P

430 450 470  
 CACGTCCTCTCCAGGAAGGGACCCCGGGTCCACGAACTGCCCACGCCCTCTCCAGGAGGGG  
 R P L Q E G T R V H E L P T P S P G G D

490 510 530  
 ACCCGGGTTCACGAGCTGCCCACGTCGTCAACGGGAAGGGACCCCGGGTCCACGAGCTGCC  
 P G P R A A H V V N G K G P G S T S C P

Figure 7A



550 570 590  
 CACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCACGCGCTCTCCAGGAGGGG  
 R P L Q E G T R V H E L P T R S P G G D

610 630 650  
 ACACCGGGTTCACGAGCTGCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTG  
 T G F T S C P R P L Q E G T P G S R A A

670 690 710  
 CCCACGTCCTCTCCAGGAGGGGACACCGGGTTCACGAGCTGCCACGTCCTCTCCAGGAG  
 H V L S R R G H R V H E L P T S S P G G

730 750 770  
 GGGACACCGGGTTCACGAGCTGCCACGCCCTCTCCAGGAGGGGACACCGGGTTCACGAG  
 D T G F T S C P R P L Q E G T P G S R A

790 810 830  
 CTGCCCACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCACGTCCTCTCCAGG  
 A H V L S R K G P G S T S C P R P L Q E

850 870 890  
 AGGGGACACCGGGTTCACGAGCTGCCACGCACTTTCCAGGAAGGGACCCCGGGTTCAGG  
 G T P G S R A A H A L S R K G P R V Q V

910 930 950  
 TCTCCTGCCGGCCACATCGTGCCTTTGTGTAAATCAGAAGAAAGATGAGGAACAGGCC  
 S C R P T S C L C V N Q K K D E E Q A L

970 990 1010  
 TCCTCTCTCTCCAGGCAGGCTTTGGTGGAGGGGCTGGATCTCCTGCCGCACCTTCCCTGG  
 L S L Q A G F G G G A G S P A A P S L A

1030 1050 1070  
 CAGGGCACCCCTGTGCTTGAGCCCCAGAACTGCAGGCGGCCGGCAGAGAAGGGGTCCATGA  
 G H P V L E P Q N C R R P A E K G S M M

Figure 7B

1090 1110 1130  
TGGCGCCTCGGTGCGCAGCCTTGGACCTGCCCCATGGACCTGGGAACCTCCCGGCTCTT  
A P R C A A L D L P P W T W E P P G S S

1150 1170 1190  
CCCACTCGGGAAAGGAAGGCTCTGGGCATGGAGGTCGGCCAGGCCCATCCCCGTACCCT  
H S G K E G S G H G G R P G P I P V P W

1210 1230 1250  
GGCCCTTCTTCTGCTTCCTGTTTGTCACTGCCCCGGGGCCTTTGCACCTGCATTCCCTC  
P F F L L P V C H C P G A F A P A F P L

1270 1290 1310  
TCTCTGTGAGTGTCTCTGGGGCCCGTTACCCACGTCACCGTCCCAGGATACCTTTTCTTTT  
S V S V L G P V T H V T V P G Y L F F S

1330 1350 1370  
CTTTCTCTCTCTCCAGCTTTATTGAGGTATAGTTGACAATTCAGGACGGTGTGCACTCAA  
F S L S S F I E V \*

1390 1410 1430  
GGTATGCAGCATCACAACCTGACACACGTAGGCATTGTGAAATGAGTCCCACAAATTGGGC

1450 1470 1490  
TAATTAACACACCCATCACCTTACATGGTTACTTCTTTCTGTGGTGAGAACTAAATTT

1510 1530 1550  
TAAATAGAGGACACACAGCCTGGGCAACATAGTGAGACCCTGTCTCTACAAATATAAAAAA

1570 1590 1610  
AATTATCTGGACGTGGTGGTGCACACCTGTGGTCCCAGCTACTTGGGAAGCTGAGGCTGG

1630 1650 1670  
AGAATCACTTGAGCCTGGGAGGCGGAGGTTGCGGTGCACTCCAGCCTGGGCGACAGAGGG

Figure 7C

1730

AAAA

Figure 7D

# Genes

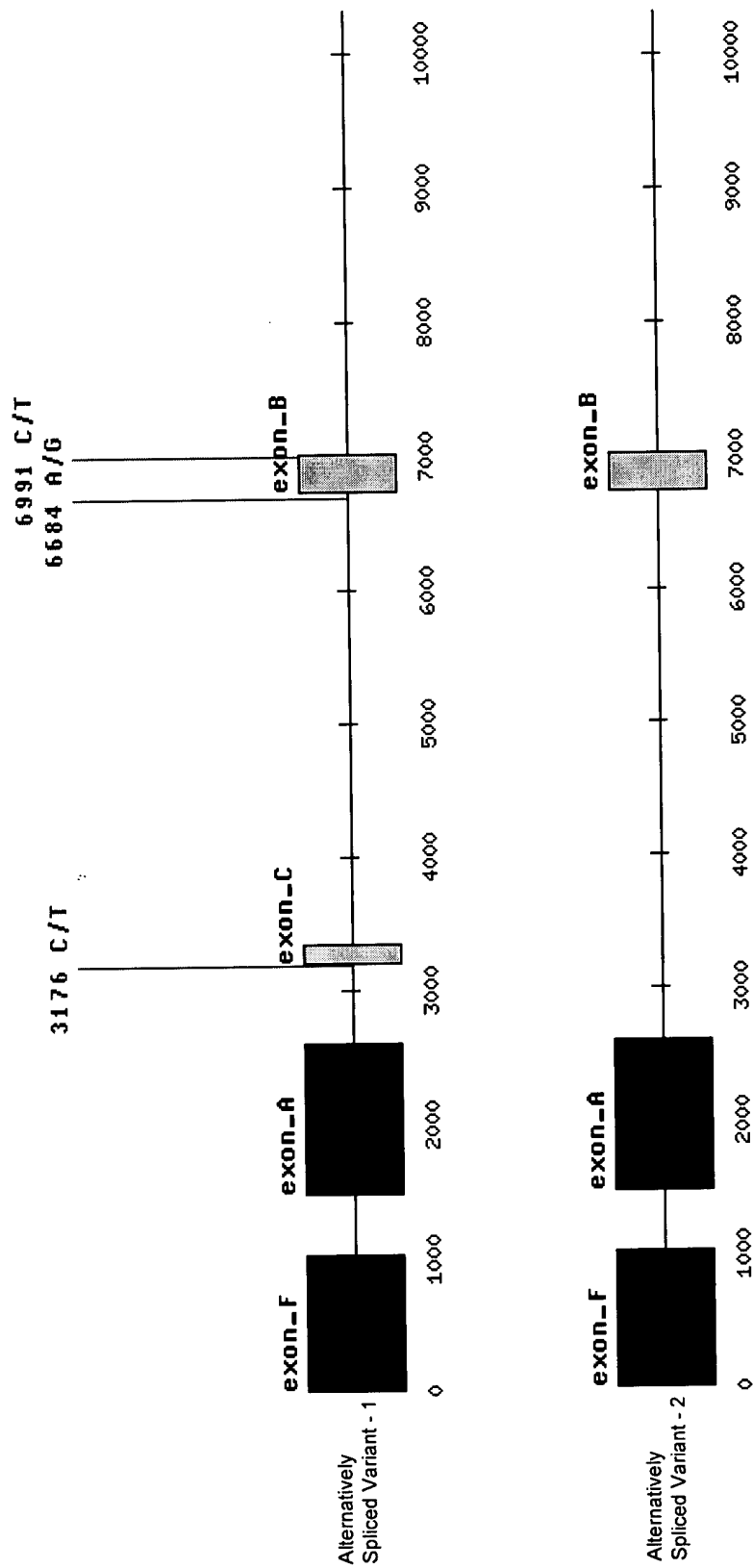


Figure 8A

Alternatively Spliced Variants from Gene 214

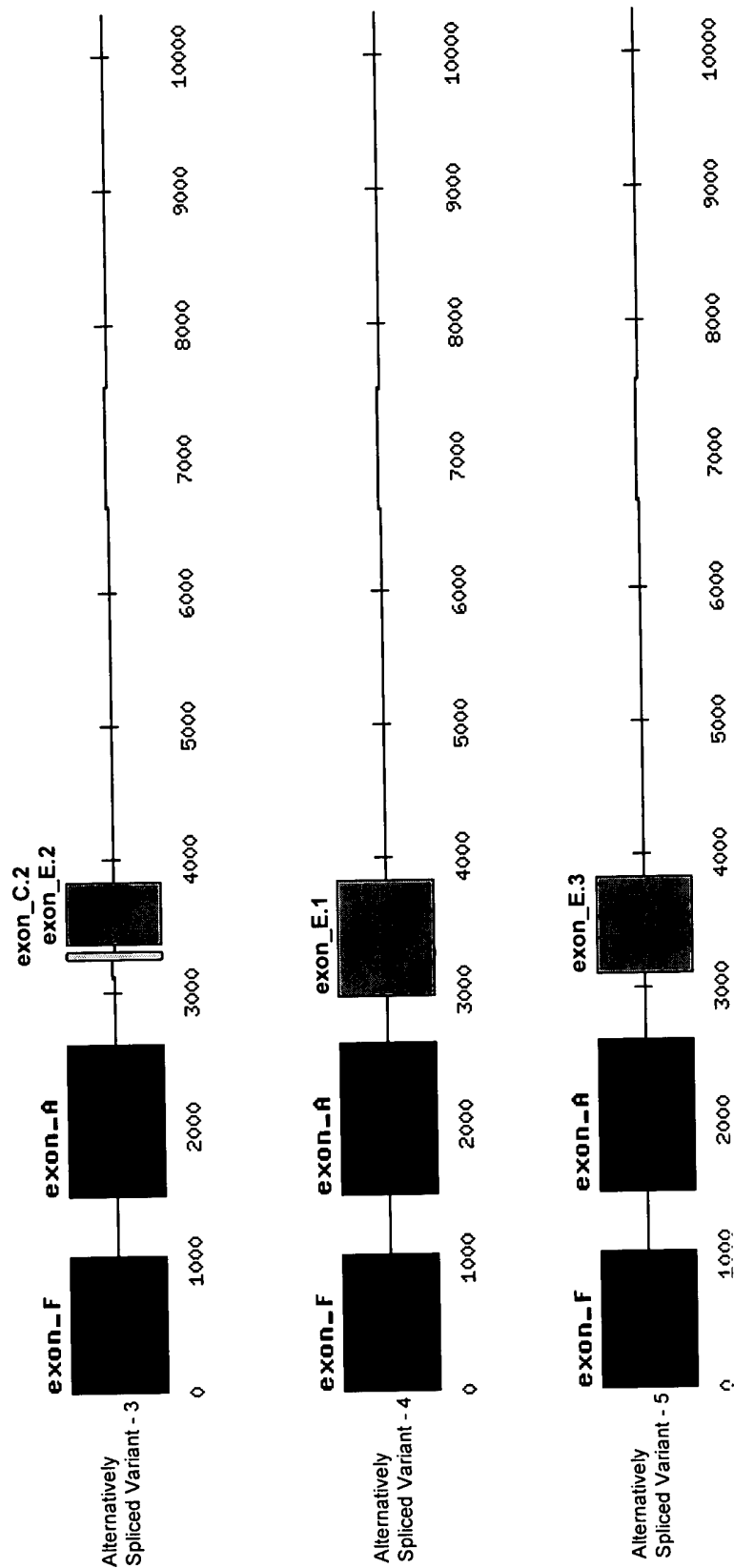
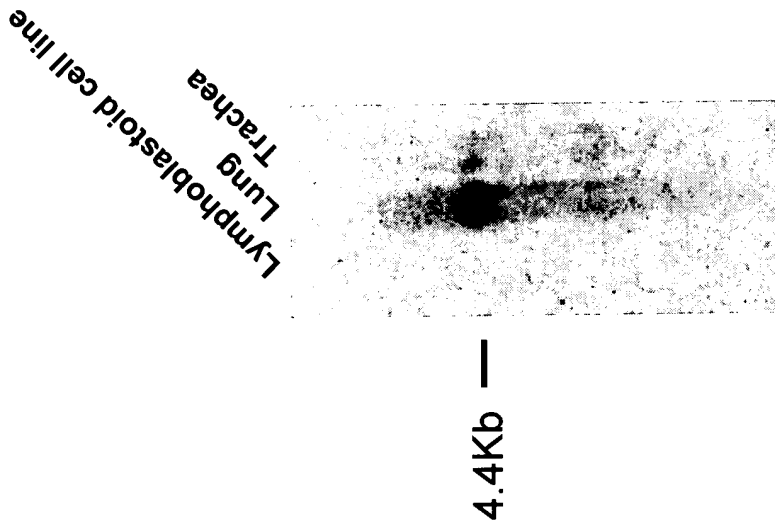


Figure 8B

Alternately Spliced Variants from Gene 214



Northern blot analysis of Gene 214

Figure 9

>Gene 214 Exon\_A  
 TCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCG  
 TCTCCAGGAAGGGACCCCGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCGGG  
 TCCACGAGCTGGCCACGTCCTCTGCAGGAAGGGACCCCGGGTCCACGAGCTGCCCACGTC  
 CTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCC  
 GGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTCCACGAAGTGGCCAC  
 GTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAGGGGAC  
 ACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCATGAGCTGCC  
 CACGTCCTCTCCAGGAAGGGACCCCGGTCCACGAAGTGGCCACGCCCTCTCCAGGAGGGG  
 ACCCGGTTCACGAGCTGCCCACGTCGTCACGGGAAGGGACCCCGGTTCACGAGCTGCC  
 CACGTCCTCTCCAGGAAGGGACCCCGGTCCACGAAGTGGCCACGCCCTCTCCAGGAGGGG  
 ACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGTTCACGAGCTG  
 CCCACGTCCTCTCCAGGAGGGGACACCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAG  
 GGGACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAGGGGACACCGGGTTCACGAG  
 CTGCCCACGTCCTCTCCAGGAAGGGACCCCGGTTCACGAGCTGCCCACGTCCTCTCCAGG  
 AGGGGACACCGGGTTCACGAGCTGCCCACGCACTTTCAGGAAGGGACCCCGGTTCAGG  
 TCTCTGCGCGCCACATCGTGCCTTTGTGTAAATCAGAAGAAAGATGAGGAACAGGCC  
 TCCTCTCTCCAGGAGGGCTTTGGTGGAGGGGCTGGATCTCTGCGCACCTTCCCTGG  
 CAGGGCACCTGTGCTTGAGCCCCAGAACTGCAGGCGGCCGAGAGAAGGGGTCCATGA  
 TGGCGCCTCGGTGCGCAGCCTTGACCTGCCCCATGGACCTGG

>Gene 214 Exon\_B  
 AGACAGGGTTTCTCCTCATTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGACGATCCAC  
 CTGCCTCAGCCTCCCGAAGTGTTGGGATTACAGGCACGAGCCACTGTGCCCCGGCCATCAT  
 TCCTTTTTTACTGCTGACTAATAGTCTGCTGTGTGAATCCACCGCTAGAAACCCACTCATC  
 AGTTGATGGTCATGTGGGTGCTTCTGCTATTGCTTATTATGAACAGTGTCTGGAATAAA  
 CGTTCCTGTGCACTCTTGGGCATACGCCTAGGAGTGGAAGTGTCTGGGTCT

>Gene 214 Exon\_C  
 GAACCTCCCGGCTCTTCCCACTCGGGAAAGGAAGGCTCTGGGCATGGAGGTGGGCCAGGC  
 CCCATCCCGGTACCTTGGCCCTTCTTCTGCTTCTGTTTGTCACTGCCCCGGGGCCTTT  
 GCACCTGCATTCCCTCTCTCT

>Gene 214 Exon\_C.2  
 GAACCTCCCGGCTCTTCCCACTCGGGAAAGGAAGGCTCTGGGCATGGAG

>Gene 214 Exon\_E.1  
 ATGCCAGTGATGCCTGAGGTCTGCAGGGCAGTGCATACGCTCACCGCCTGGCCGCTCAGG  
 AGCCTGTGCTTGACCCCCAAATCCGCCCCCAACTCCCTGTTACCGGCTCACTCCTTCCA  
 TGAGGGGCCTTCCCCAGGGACAGCCGATGCTCTCCTGATGGCTCCTGCCCTTGACAGAGTG  
 CTGCCCCCGCCTGCCCACCTGGCCTGGACCTCGCCTGAGCCCCCTCAGGGCTCTGCGCC  
 ACCTCAACCCAGGCGTTTGTTCGCGAGGAACCTCCCGGCTCTTCCCACTCGGGAAAGGAA  
 GGCTCTGGGCATGGAGGTGGGCCAGGCCCATCCCCGTACCTGGCCCTTCTTCTGCTT  
 CCTGTTTGTCACTGCCCCGGGGCCTTTGCACCTGCATTCCCTCTCTCTGTGAGTGTCTTG  
 GGGCCCGTTACCCACGTCACCGTCCAGGATACCTTTTCTTTTCTTCTCTCTCCAGC  
 TTTATTGAGGTATAGTTGACAATTGAGACGGTGTGCACTCAAGGTATGACGATCACAA  
 CCTGACACACGTAGGCATTGTGAAATGAGTCCACAAATTGGGCTAATTAACACACCCATC  
 ACCTTACATGGTTACTTCTTTCTGTGGTGAGAACACTAAATTTTAAATAGAGGACACACA  
 GCCTGGGCAACATAGTGAGACCCTGTCTCTACAAATATAAAAAAATTAATCTGGACGTGGT  
 GGTGCACACCTGTGGTCCAGCTACTTGGGAAGCTGAGGCTGGAGAATCACTTGAGCCTG  
 GGAGGCGGAGGTTGCGGTGCACTCCAGCCTGGGCGACAGAGGGAGGCCCTATCTCAAAAT  
 AAATAAATAAAGGACACATTCTTATC

FIGURE 10A

>Gene 214 Exon E.2

CTTTATTGAGGTATAGTTGACAATTCAGGACGGTGTGCACTCAAGGTATGCAGCATCACA  
ACCTGACACACGTAGGCATTGTGAAATGAGTCCCACAATTGGGCTAATTAAACACACCCAT  
CACCTTACATGGTTACTTCTTTCTGTGGTGAGAACACTAAATTTTAAATAGAGGACACAC  
AGCCTGGGCAACATAGTGAGACCCTGTCTCTACAAATATAAAAAAATTATCTGGACGTGG  
TGGTGCACACCTGTGGTCCCAGCTACTTGGGAAGCTGAGGCTGGAGAATCACTTGAGCCT  
GGGAGGCGGAGGTTGCGGTGCACTCCAGCCTGGGCGACAGAGGGAGGCCCTATCTCAAAA  
TAAATAAATAAAGGACACATTCTTATC

>Gene 214 Exon E.3

GAACCTCCCGCTCTTCCCCTCGGGAAAGGAAGGCTCTGGGCATGGAGGTCGGCCAGGC  
CCCATCCCCGTACCCTGGCCCTTCTTCTGCTTCTGTTTGTCACTGCCCCGGGGCCTTT  
GCACCTGCATTCCCTCTCTCTGTGAGTGTCTGGGGCCCGTTACCCACGTACCCGTCCCA  
GGATACCTTTTCTTTTCTTTCTCTCTCTCCAGCTTTATTGAGGTATAGTTGACAATTGAG  
GACGGTGTGCACTCAAGGTATGCAGCATCACAACCTGACACACGTAGGCATTGTGAAATG  
AGTCCCACAATTGGGCTAATTAACACACCCATCACCTTACATGGTTACTTTCTGTGG  
TGAGAACACTAAATTTTAAATAGAGGACACACAGCCTGGGCAACATAGTGAGACCCTGTC  
TCTACAAATATAAAAAAATTATCTGGACGTGGTGGTGCACACCTGTGGTCCCAGCTACTT  
GGGAAGCTGAGGCTGGAGAATCACTTGAGCCTGGGAGGCGGAGGTTGCGGTGCACTCCAG  
CCTGGGCGACAGAGGGAGGCCCTATCTCAAAATAAATAAATAAAGGACACATTCTTATC

>Gene 214 Exon F

CGGGCGTGTATATCTCTTCATAGAGAGCGCTCAGACAGCGTGCGTTAATCTGCGTCGATA  
TATAGAGATCTTTATCACTGAGTAGATAGAACGTACATGAATGTACGAACAGTCCAGACG  
AGTAACTTGACTAGGATAAGATAGACAGTACCAACTAATGAGACAAGAAGAGGGAATCAT  
ATAGAATCATGTAGTCTGAGTCTAGCGAGTGTGACATGATCACAAGCGAAATACAGACT  
ATGAGAAGAGGTAGAAATAATAAGTANACTGAGAAGAGAGGTCATATGTACATACAAATC  
AGTAAAGCAATAGAAATTGAATACATTATAAGCCACAGTTACAGAATTAGCCTAATTTAA  
CAACCATGGCAAGCGAGTTATATCAAACATAGAAGAGTAAACTCTATCGACCATGGGTAG  
GAACGAATAAAGGCGTCGAGAAGACAATAAGAATGCGTGTTAAACAGCAATACAAGAGAA  
TAGCACCACTGAAGCAGACCAAGGCGTCACCGGGGAAGTAGGGAAGAGGCACCTCACAA  
GGAGAGGAAAGGGCAGTCCTGATTTTGAAAATTTTCAGTGAAAAGACAGTGTTGTTCCCGG  
AGGCAGCTTAGTGATCCCGCATCGACTCTGAAGAGGACCCTGAGGGTAGGGGATTTTGG  
GCCTGACCGGCCTATGCTGAACGCCCCACCGGGAATTCAGGGAGAAACACGGGGCCCCGGC  
TTCCAGGAGAGCAGCCAGGCCACAGCCCTGAGGACGGGCAAACCCACCCAGGCACGGTG  
AGAGGGAGGCCGCCAGGCCTGGGGCCTGGCGGCAGGGGATGAAGTGGACCAAGAGCCCCG  
CAAATCCTAACGTGGGTGAGCAGTGAGCCTGTGTGGCTGCGAGTGGCTCCGTTTTGGGGC  
TGTTTGTTCCTGCAGCAAATGATGCCAGCCCTGACGGAACCAGTGCACGTCCACCACGAG  
CTGCCCACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCACGTCCTCTCCAGG  
AAGGGACC

FIGURE 10B